IN THE SPECIFICATION

On page 1, immediately above line 1, please insert the following paragraph:

The present application is a national phase entry under 35 U.S.C. § 371 of International Application No. PCT/1B04/02491 filed July 5, 2004, which claims priority under 35 USC 119(d) to European application no. 03292057.0 filed December 8, 2003 and European application no. 03291677.7 filed July 4, 2003, all of which are incorporated herein by reference.

Please delete the paragraph beginning on page 1, line 4 as follows:

~~The invention relates to a method of producing a double low restorer line of Brassica napus for Ogura cytoplasmic male sterility (cms) presenting a radish introgression carrying the Rfo restorer gene deleted of the radish Pgi-2 allele and recombined with the Pgi-2 gene from Brassica oleracea, and having a good agronomic value characterized by female fertility, a good transmission rate of Rfo and a high vegetative vigour. The invention relates also to a method of forming Brassica napus hybrid seeds and progeny thereof and to the use of markers for selection.~~

On page 1, immediately above current line 12, please insert the following:

Background of the Invention

On page 1, immediately above current line 24, please insert the following:

Summary of the Invention

On page 5, immediately above line 39, please insert the following:

Brief Description of the Drawings

On page 8, immediately before line 1, please insert the following:

Detailed Description of the Invention

Please amend the paragraph beginning on page 1, line 24 as follows:

A first object of the present invention relates to a method of producing double low restorer lines of Brassica napus for Ogura cms presenting ~~radis~~ radish introgression carrying the Rfo restorer gene deleted of the radish Pgi-2 allele and recombined with the Pgi-2 gene from Brassica oleracea, and having a good agronomic value characterised by female fertility, a good transmission rate of Rfo and a high vegetative vigour, said method including the step of:

a) crossing double low cms lines of spring Brassica napus comprising a deleted radish insertion with the double low line of spring Drakkar for forming heterozygous restored plants of Brassica napus,

b) irradiating before meiosis the heterozygous restored plants obtained in step a) with gamma ray irradiation,

c) crossing pollen from flowers obtained in step b) with the cms double low spring Wesroona line,

d) testing the progeny for vigour, female fertility and transmission rate of the cms gene,

e) selecting progeny lines.

Please amend the paragraph beginning on page 2, line 10 as follows:

~~A method according to claim 1~~The above method, wherein the irradiation dose in step b) is 65 Gray during 6 mn.

Please amend the paragraph beginning on page 2, line 29 as follows:

Another object of the present invention relates to Brassica napus hybrid plants and progeny thereof obtained though the steps of:

a) providing a restorer line produced according to the above methodclaim 1 and bred to be homozygous,

b) using said restorer line in a hybrid production field as the pollinator,

c) using cms sterile plants in a hybrid production field as the hybrid seed producing plant, and

d) harvesting the hybrid seed from the male sterile plant.

Please amend the paragraph beginning on page 7, line 12 as follows:

- Figure 16 (16 et and 16bis) illustrates Arabidopsis, Radish and B.rapa BolJon markers. There are aligned with DB sequences of Arabidopsis (AC007190end-AC011000beginning), the B.oleracea EMBH959102 end and EMBH448336 begining and representative consensus sequences of the SG129markers band 1 and 2 in B.napus (in Drakkar and Samourai respectively).

Please amend the paragraph beginning on page 7, line 26 as follows:

- Figure 17 (17 et and 17bis) illustrates the localisation of Pgi-2 primers on the Arabidopsis th MJB21.12 sequence.

Please delete the paragraph beginning on page 7, line 28 as follows:

~~- Figure 18 illustrates the BolJon primers localisation on the mipsAt162850 gene and overlapping area of AC007190 and~~

~~AC011000 Arabidopsis th clones. Alignment with the Arabidopsis BolJon PCR product (740bp) is presented.~~

Please amend the paragraph beginning on page 8, line 12 as follows:

Genotypes: The 'R211' line with a deleted radish insertion was crossed to the spring low glucosinolates (GLS) rapeseed 'Drakkar' to produce a F1 progeny ('R211*Dk'). The spring low GLS cms line 'Wesroona' (australian origin) was used for following crosses. The following lines were~~Were~~ used as controls~~control~~ in molecular analyses: Winter restored lines derived from 'Samourai' carrying the complete ('RRH1') or incomplete ('R113') introgression as well as European radish line7, Asiatic restored radish D81, hybrid Brasica napus~~*~~, wild radish, Brassica oleracea, and B.rapa cv Asko, Arabidopsis thaliana.

Please amend the paragraph beginning on page 8, line 19 as follows:

Gamma ray irradiation: Whole flowering plants were treated with gamma rays from a Co60 source in a controlled area. Sublethal~~Subletal~~ dose of~~fo~~ 65 Gray was applied before meiosis~~meioses~~.

Please amend the paragraph beginning on page 8, line 27 as follows:

Phenotypic selection: Three visual criteria were scored (on a 1 to 5 scale) over 2 years in field assays, on 1200 F2 offsprings plus 44 controls (82 330 ~~quoted~~ plants):

1-Vegetative vigour,

2- Normality of the ratio of fertile /sterile plants in the F2 segregation, and

3- Female fertility (pod development and seed set).

Advanced selfed generations of the selected families were obtained either in field or greenhouse and produced homozygous lines (F4) for further analysis.

Please amend the paragraph beginning on page 9, line 9 as follows:

We choose one low GLS spring homozygous restorer line, 'R211', already exhibiting deletions in the introgression (Delourme R. and Eber F. 1992. *Theor Appl Genet* 85: 222-228. Delourme R et al 1998. *Theor Appl Genet* 97: 129-134. Delourme R. et al 1999. *10th Int. Rapeseed Congress, Canberra.)*. Several molecular markers are missing on either side of Rfo, such as spATCHIA (Fourmann M et al 2002. *Theor Appl. Genet.* 105:1196-1206), spSG91 (Giancola S et al 2003 *Theor Appl. Genet. (in press)*). 'R211' lost the isozyme expression of the Pgi-2 allele of the radish gene but also the one of Pgi-2 allele of B.oleracea genome (1,2). Moreover, the homozygous 'R211' shows linked negative traits such as low vigour and very poor seed set. We hypothesised that these plants~~plant~~ lack a rapeseed chromosomal segment. The fertile ratio in F2 progenies derived from this material is lower than expected (64% instead of 75%). We initiated the program from this 'R211' line and tried to force recombination between the Rfo carrying introgression from this deleted line and the rapeseed homologous chromosome from a double low B. napus line.

Please amend the paragraph beginning on page 10, line 25 as follows:

This marker had the specificity of the PGIol marker but amplifying a longer part such as PGIint~~as for PGIint one~~.